In the claims:

1. (Currently amended) A method to identify the polypeptide correlating with a phenotype of interest, wherein the polypeptide specifically recognizes and binds a serum antibody, said method comprising identifying the polypeptide correlating with a phenotype of interest, wherein the polypeptide specifically recognizes and binds a serum antibody obtained from a subject common to a list of characterized genes, wherein said genes are differentially expressed in one or more relevant cells or tissues and a list of characterized polypeptides, thereby identifying said polypeptide correlating with said phenotype of interest.

2. (Original) The method of claim 1, wherein the genes of the list are characterized by properties of the gene product, wherein the said properties are selected from the group consisting of specific reactivity with the serum antibody, highly expressed in the relevant cell line or tissue, little or no detectable expression in the relevant cell line or tissue, and uniquely expressed in the relevant cell line or tissue.

3. (Original) The method of claim 2, wherein two or more properties characterize the properties of the gene product.

4. (Original) The method of claim 2, further comprising the property of molecular weight.

5. (Original) The method of claim 3, further comprising the property of molecular weight.

6. (Currently amended) The method of claim 1, wherein the list of characteristics of the proteins of the list is a selected from mass, reactivity with the serum antibody, peptidase digestion pattern, enzymatic digestion pattern and MOALDI-TOF selection criteria.

7. (Original) The method of claim 6, wherein two or more properties characterize the properties of the gene product.

8. (Original) The method of claim 6, further comprising the property of molecular weight.

9. (Original) The method of claim 7, further comprising the property of molecular weight.

10. (Currently amended) The method of claim 6, wherein M~~O~~ALDI-TOF selection criteria are selected from the group consisting database selection, species, type of digest, ~~CNBr,~~ number of miscleavages, molecular weight range, contamination indication, and mass accuracy.